AMENDMENTS TO THE CLAIMS

Please replace all prior versions, and listings, of claims in the application with the following list of claims:

1. (Currently amended) A method for analyzing polymer intensity data from a sample comprising

obtaining individual intensity profiles from individual labeled polymers contained in the sample,

wherein individual intensity profiles are obtained by detecting signals from the individual labeled polymers,

aligning individual intensity profiles from individual labeled polymers with respect to an alignment reference point,

wherein the alignment reference point is a center of molecule reference point,

combining aligned individual intensity profiles to generate a sample population profile,

selecting a peak in the sample population profile and obtaining individual intensity profiles that contribute to the peak,

combining individual intensity profiles that contribute to the peak to generate a peak profile, and

comparing the peak profile with the sample population profile,

wherein the individual intensity profile is stored as an intensity versus length profile or an intensity versus time histogram, and

wherein the polymers are labeled with a sequence specific probe.

2. (Original) The method of claim 1, wherein the sample contains a heterogeneous mixture of polymers.

3. (Original) The method of claim 2, wherein the heterogeneous mixture of polymers comprises differentially sized fragments of a parent polymer.

4. (Original) The method of claim 2, wherein the heterogeneous mixture of polymers comprises polymers with different sequences.

5. (Canceled)

6. (Original) The method of claim 1, wherein the intensity data is fluorescence intensity data and intensity profiles are fluorescence intensity profiles.

7. (Canceled)

8. (Original) The method of claim 1, wherein the polymers are labeled with a sequence non-specific label.

9. (Original) The method of claim 1, wherein the method is implemented on a computer.

10. (Original) The method of claim 1, wherein the polymer is a nucleic acid.

11. (Original) The method of claim 10, wherein the nucleic acid is DNA or RNA.

12. (Original) The method of claim 11, wherein the DNA is genomic nuclear DNA, mitochondrial DNA or cDNA.

13. (Withdrawn) The method of claim 11, wherein the RNA is mRNA.

14-17. (Canceled)

18. (Original) The method of claim 1, wherein the intensity profiles are obtained from individual polymers in flow.

19. (Withdrawn) The method of claim 1, wherein the intensity profiles are obtained from individual polymers fixed to a solid support.

20. (Withdrawn) The method of claim 1, wherein the population profile is a cumulative population profile.

21. (Previously presented) The method of claim 1, wherein the sample population profile is an average population profile.

22. (Withdrawn) The method of claim 1, wherein the peak profile is a cumulative peak profile.

23. (Original) The method of claim 1, wherein the peak profile is an average peak profile.

24. (Original) The method of claim 1, wherein the peak is selected based on intensity.

25. (Original) The method of claim 1, wherein the peak is selected based on the presence of its mirror image peak in the population profile.

26. (Original) The method of claim 1, wherein polymers in the sample are sorted according to size prior to aligning individual intensity profiles.

27. (Currently amended) The method of claim 1, wherein a peak profile that resembles the sample population profile indicates a non-oriented profile.

28. (Original) The method of claim 1, wherein a peak profile that consists of a subset of peaks from the sample population profile indicates a putative oriented profile.

29. (Currently amended) A method for analyzing polymer intensity data from a sample comprising

obtaining individual intensity profiles from individual labeled polymers contained in the sample,

wherein individual intensity profiles are obtained by detecting signals from the individual labeled polymers,

aligning individual intensity profiles from individual labeled polymers with respect to an alignment reference point,

combining aligned individual intensity profiles to generate a sample population profile,

selecting a peak in the sample population profile and obtaining individual intensity profiles that contribute to the peak,

combining individual intensity profiles that contribute to the peak to generate a peak profile, and

comparing the peak profile with the sample population profile,

wherein the individual intensity profile is stored as an intensity versus length profile or an intensity versus time histogram,

wherein the polymers are labeled with a sequence specific probe,

wherein a peak profile that consists of a subset of peaks from the sample population profile indicates a putative oriented profile,

~~The method of claim 28, further comprising~~ inverting the putative oriented profile to generate a putative inverted profile,

combining the putative oriented profile with the putative inverted profile to generate a putative non-oriented profile, and

comparing the putative non-oriented profile with the population profile,

wherein a putative non-oriented profile that is identical to the population profile indicates that the putative oriented profile is an oriented profile, that the putative inverted profile is an inverted profile, and that the putative non-oriented profile is a non-oriented profile.

30. (Currently amended) A method for analyzing polymer intensity data from a sample comprising

obtaining individual intensity profiles from individual labeled polymers contained in the sample,

wherein individual intensity profiles are obtained by detecting signals from the individual labeled polymers,

aligning individual intensity profiles from individual labeled polymers with respect to an alignment reference point,

combining aligned individual intensity profiles to generate a sample population profile,

selecting a peak in the sample population profile and obtaining individual intensity profiles that contribute to the peak,

combining individual intensity profiles that contribute to the peak to generate a peak profile, and

comparing the peak profile with the sample population profile,

wherein the individual intensity profile is stored as an intensity versus length profile or an intensity versus time histogram, and

wherein the polymers are labeled with a sequence specific probe,

wherein a peak profile that consists of a subset of peaks from the sample population profile indicates a putative oriented profile,

~~The method of claim 28, further comprising~~ determining whether individual peaks in the peak profile have corresponding mirror image peaks in the population profile when the alignment reference point is a center of molecule reference point.

31. (Original) The method of claim 30, wherein the presence of corresponding mirror images indicates the putative oriented profile is an oriented profile.

32. (Currently amended) A method for analyzing polymer intensity data from a sample comprising

obtaining individual intensity profiles from individual labeled polymers contained in the sample,

wherein individual intensity profiles are obtained by detecting signals from the individual labeled polymers,

aligning individual intensity profiles from individual labeled polymers with respect to an alignment reference point,

combining aligned individual intensity profiles to generate a sample population profile,

selecting a peak in the sample population profile and obtaining individual intensity profiles that contribute to the peak,

combining individual intensity profiles that contribute to the peak to generate a peak profile, and

comparing the peak profile with the sample population profile,

wherein the individual intensity profile is stored as an intensity versus length profile or an intensity versus time histogram, and

wherein the polymers are labeled with a sequence specific probe,

wherein a peak profile that consists of a subset of peaks from the sample population profile indicates a putative oriented profile,

~~The method of claim 28, further comprising~~ determining whether the oriented peak has a corresponding mirror image peak in the sample population profile when the alignment reference point is a center of molecule reference point.

33. (Original) The method of claim 32, further comprising obtaining individual intensity profiles that contribute to the mirror image peak, and combining individual intensity profiles that contribute to the mirror image peak to generate a mirror image peak profile.

34. (Original) The method of claim 33, further comprising comparing the mirror image peak profile with the sample population profile.

35. (Original) The method of claim 34, further comprising determining whether the mirror image peak profile is a mirror image of the peak profile.

36. (Original) The method of claim 35, further comprising inverting and combining the mirror image peak profile with the peak profile provided the mirror image peak profile is a mirror image of the peak profile.

37. (Withdrawn) The method of claim 33, wherein the mirror image peak profile is a cumulative mirror image peak profile.

38. (Original) The method of claim 33, wherein the mirror image peak profile is an average mirror image peak profile.

39. (Previously presented) The method of claim 28, further comprising subtracting the peak profile from the sample population profile.

40. (Original) The method of claim 35, further comprising subtracting the mirror image peak profile from the sample population profile.

41. (Original) The method of claim 35, further comprising subtracting the peak profile and the mirror image peak profile from the sample population profile.

42. (Original) The method of claim 41, further comprising determining whether additional peaks remain in the sample population profile following subtraction of the peak profile and the mirror image peak profile.

43. (Original) The method of claim 42, wherein the presence of additional peaks is indicative that the sample comprised different polymers.

44. (Original) The method of claim 1, wherein the polymer is completely stretched.

45. (Original) The method of claim 1, wherein the polymer is partially stretched.

46. (Original) The method of claim 31, further comprising inverting the oriented profile, combining the oriented profile with the inverted profile to generate a non-oriented profile, and comparing the non-oriented profile with the sample population profile.

47. (Withdrawn) The method of claim 8, wherein the sequence non-specific label is a backbone label.

48. (Withdrawn) The method of claim 47, wherein the alignment reference point is a center of molecule reference point.

49. (Withdrawn) The method of claim 48, wherein the center of molecule reference point is the midpoint of an individual profile.

50. (Original) The method of claim 1, wherein the peak is visible in an intensity versus length profile.

51. (Original) The method of claim 1, wherein the peak corresponds to bin counts.

52. (Original) The method of claim 1, wherein the polymer is uniformly stretched.

53. (Original) The method of claim 1, wherein the sample comprises polymers embedded in a gel matrix.

54. (Original) The method of claim 31, further comprising subtracting the peak profile from the sample population profile.

55. (Currently amended) A method for analyzing polymer intensity data from a sample comprising

obtaining individual intensity profiles from individual labeled polymers contained in the sample,

wherein individual intensity profiles are obtained by detecting signals from the individual labeled polymers,

aligning individual intensity profiles from individual labeled polymers with respect to an alignment reference point,

combining aligned individual intensity profiles to generate a sample population profile,

selecting a peak in the sample population profile and obtaining individual intensity profiles that contribute to the peak,

combining individual intensity profiles that contribute to the peak to generate a peak profile, and

comparing the peak profile with the sample population profile,

wherein the individual intensity profile is stored as an intensity versus length profile or an intensity versus time histogram,

wherein a peak profile that resembles the population profile indicates a non-oriented profile.

56. (New) A method for analyzing polymer intensity data from a sample comprising

obtaining individual intensity profiles from individual labeled polymers contained in the sample,

wherein individual intensity profiles are obtained by detecting signals from the individual labeled polymers,

aligning individual intensity profiles from individual labeled polymers with respect to an alignment reference point,

combining aligned individual intensity profiles to generate a sample population profile,

selecting a peak in the sample population profile based on the presence of its mirror image peak in the population profile and obtaining individual intensity profiles that contribute to the peak,

combining individual intensity profiles that contribute to the peak to generate a peak profile, and

comparing the peak profile with the sample population profile,

wherein the individual intensity profile is stored as an intensity versus length profile or an intensity versus time histogram, and

wherein the polymers are labeled with a sequence specific probe.

57. (New) A method for analyzing polymer intensity data from a sample comprising

obtaining individual intensity profiles from individual labeled polymers contained in the sample,

wherein individual intensity profiles are obtained by detecting signals from the individual labeled polymers,

aligning individual intensity profiles from individual labeled polymers with respect to an alignment reference point,

combining aligned individual intensity profiles to generate a sample population profile,

selecting a peak in the sample population profile and obtaining individual intensity profiles that contribute to the peak,

combining individual intensity profiles that contribute to the peak to generate a peak profile, and

comparing the peak profile with the sample population profile,

wherein the peak profile that resembles the sample population profile indicates a non-oriented profile,

wherein the individual intensity profile is stored as an intensity versus length profile or an intensity versus time histogram, and

wherein the polymers are labeled with a sequence specific probe.